

1652

RAW SEQUENCE LISTING DATE: 11/24/2000
 PATENT APPLICATION: US/09/463,705A TIME: 13:14:52

Input Set : A:\PTO.txt
 Output Set: N:\CRF3\11242000\I463705A.raw

*Does Not Comply
 Corrected Diskette Needed*

3 <110> APPLICANT: Cortes, J
 4 Fromentin, C
 5 Gaisser, S
 6 Leadlay, P
 7 Mendez, C
 8 Michel, J-M
 9 Raynal, M-C
 10 Salah-Bey, K
 11 Salas, J
 12 <120> TITLE OF INVENTION: BIOSYNTHESIS GENES & TRANSFER OF 6-DESOXYHEXOSES IN
 13 SACCHAROPOLYSPORA ERYTHRAEA AND IN STREPTOMYCES
 14 ANTIBIOTICUS AND THEIR USE
 15 <130> FILE REFERENCE: 146.1335
 16 <140> CURRENT APPLICATION NUMBER: 09/463705A
 17 <141> CURRENT FILING DATE: 2000-02-23
 18 <150> PRIOR APPLICATION NUMBER: PCT/FR98/01593
 19 <151> PRIOR FILING DATE: 1998-07-21
 20 <150> PRIOR APPLICATION NUMBER: 98/07411
 21 <151> PRIOR FILING DATE: 1988-06-12
 22 <150> PRIOR APPLICATION NUMBER: 97/09458
 23 <151> PRIOR FILING DATE: 1997-07-25
 24 <160> NUMBER OF SEQ ID NOS: 61
 25 <170> SOFTWARE: PatentIn Ver. 2.1

*Format errors. Enter "hard return"
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ERRORED SEQUENCES

2865 <210> SEQ ID NO: 32<211> 24
 2866 <212> TYPE: DNA
 2867 <213> ORGANISM: Artificial sequence
 2869 <220> FEATURE:
 2870 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic oligonucleotide
 W--> 2872 <211> LENGTH:
 2872 <400> SEQUENCE: 32
 E--> 2873 atgcgcgtcg tcttctctc catg 24
 3082 <210> SEQ ID NO: 50<211> 33
 3083 <212> TYPE: DNA
 3084 <213> ORGANISM: Artificial sequence
 3086 <220> FEATURE:
 3087 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic oligonucleotide
 W--> 3089 <211> LENGTH:
 3089 <400> SEQUENCE: 50
 E--> 3090 aggagcacta gtgcgggtac tgctgacgtc ctt 33

VERIFICATION SUMMARY

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L:42 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:1, CDS LOCATION: Complement((48)..(1046))
L:48 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:1, CDS LOCATION: Complement((2322)..(3404))
L:324 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:4, CDS LOCATION: complement (4)..(1266)
L:603 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:607 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:711 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:715 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
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L:723 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:727 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:731 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:735 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
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L:797 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:801 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
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L:877 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:881 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6

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L:885 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:889 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:893 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:897 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:901 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:2872 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:2873 M:252 E: No. of Seq. differs, <211>LENGTH:Input:0 Found:24 SEQ:32
L:3089 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:3090 M:252 E: No. of Seq. differs, <211>LENGTH:Input:0 Found:33 SEQ:50